-continued

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(v i i i) POSITION IN GENOME:
(B) MAP POSITION: HUMvWFA31

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGACAGATGA TAAATACATA GGATGGATGG ATA 33

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(v i i i) POSITION IN GENOME:
(B) MAP POSITION: D9S930

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCTATGGGAA TTACAAGCAG GAAAC 25

What is claimed is:

1. A method of simultaneously determining the alleles present in at least four short tandem repeat loci from one or more DNA samples, comprising:

(a) obtaining at least one DNA sample to be analyzed,

(b) selecting a set of at least four short tandem repeat loci of the DNA sample to be analyzed which can be amplified together, wherein the at least four loci in the set are selected from the group of loci consisting of: D3S1539, D4S2368, D5S818, D7S820, D9S930, D10S1239, D13S317, D14S118, D14S548, D14S562, D16S490, D16S539, D16S753, D17S1298, D17S1299, D19S253, D20S481, D22S683, HUMCSF1PO, HUMTPOX, HUMTH01, HUMF13A01, HUMBFXIII, HUMLIPOL, HUMvWFA31;

(c) co-amplifying the loci in the set in a multiplex amplification reaction, wherein the product of the reaction is a mixture of amplified alleles from each of the co-amplified loci in the set; and

(d) evaluating the amplified alleles in the mixture to determine the alleles present at each of the loci analyzed in the set within the DNA sample.

2. The method of claim **1**, wherein the set of at least four loci co-amplified therein is a set of four loci, wherein the set of four loci is selected from the group of sets of loci consisting of:

D3S1539, D7S820, D13S317, D5S818;

D17S1298, D7S820, D13S317, D5S818;

D20S481, D7S820, D13S317, D5S818;

D9S930, D7S820, D13S317, D5S818;

D10S1239, D7S820, D13S317, D5S818;

D14S118, D7S820, D13S317, D5S818;

D14S562, D7S820, D13S317, D5S818;

D14S548, D7S820, D13S317, D5S818;

D16S490, D7S820, D13S317, D5S818;

D17S1299, D7S820, D13S317, D5S818;

D16S539, D7S820, D13S317, D5S818;

D22S683, D7S820, D13S317, D5S818;

D16S753, D7S820, D13S317, D5S818;

D3S1539, D19S253, D13S317, D20S481;

D3S1539, D19S253, D4S2368, D20S481;

D10S1239, D9S930, D4S2368, D20S481; and

D16S539, D7S820, D13S317, HUMvWFA31.

3. The method of claim **1**, wherein the set of at least four loci co-amplified therein is a set of six loci, wherein the set of six loci is selected from the group of sets of loci consisting of:

D16S539, D7S820, D13S317, D5S818, HUMCSF1PO, HUMTPOX; and

D16S539, D7S820, D13S317, D5S818, HUMF13A01, HUMFESFPS.

4. The method of claim **1**, wherein the set of at least four loci co-amplified therein is a set of seven loci, wherein the set is selected from the group of sets of loci consisting of:

D16S539, D7S820, D13S317, D5S818, HUMCSF1PO, HUMTPOX, HUMTH01; and

D16S539, D7S820, D13S317, D5S818, HUMF13A01, HUMFESFPS, HUMBFXIII.

5. The method of claim **1**, wherein the set of at least four loci co-amplified therein is a set of at least eight loci, and wherein the set is selected from the group of sets of loci consisting of:

D16S539, D7S820, D13S317, D5S818, HUMCSF1PO, HUMTPOX, HUMTH01, HUMvWFA31; and

D16S539, D7S820, D13S317, D5S818, HUMF13A01, HUMFESFPS, HUMBFXIII, HUMLIPOL.

6. The method of claim **1**, wherein the multiplex amplification reaction is done using at least four pair of primers flanking the at least four loci analyzed.

7. The method of claim **6**, additionally comprising the step of selecting pairs of primers for the multiplex amplification reaction which produce alleles from each locus that do not overlap the alleles of the other loci in the set co-amplified therein, when the alleles are separated by gel electrophoresis.

8. The method of claim **6**, wherein at least one of each of the pairs of primers used in the multiplex amplification reaction has a sequence selected from one of the groups of sequences consisting of:

SEQ ID NO:1 and SEQ ID NO:2, when one of the loci in the set is D7S820;